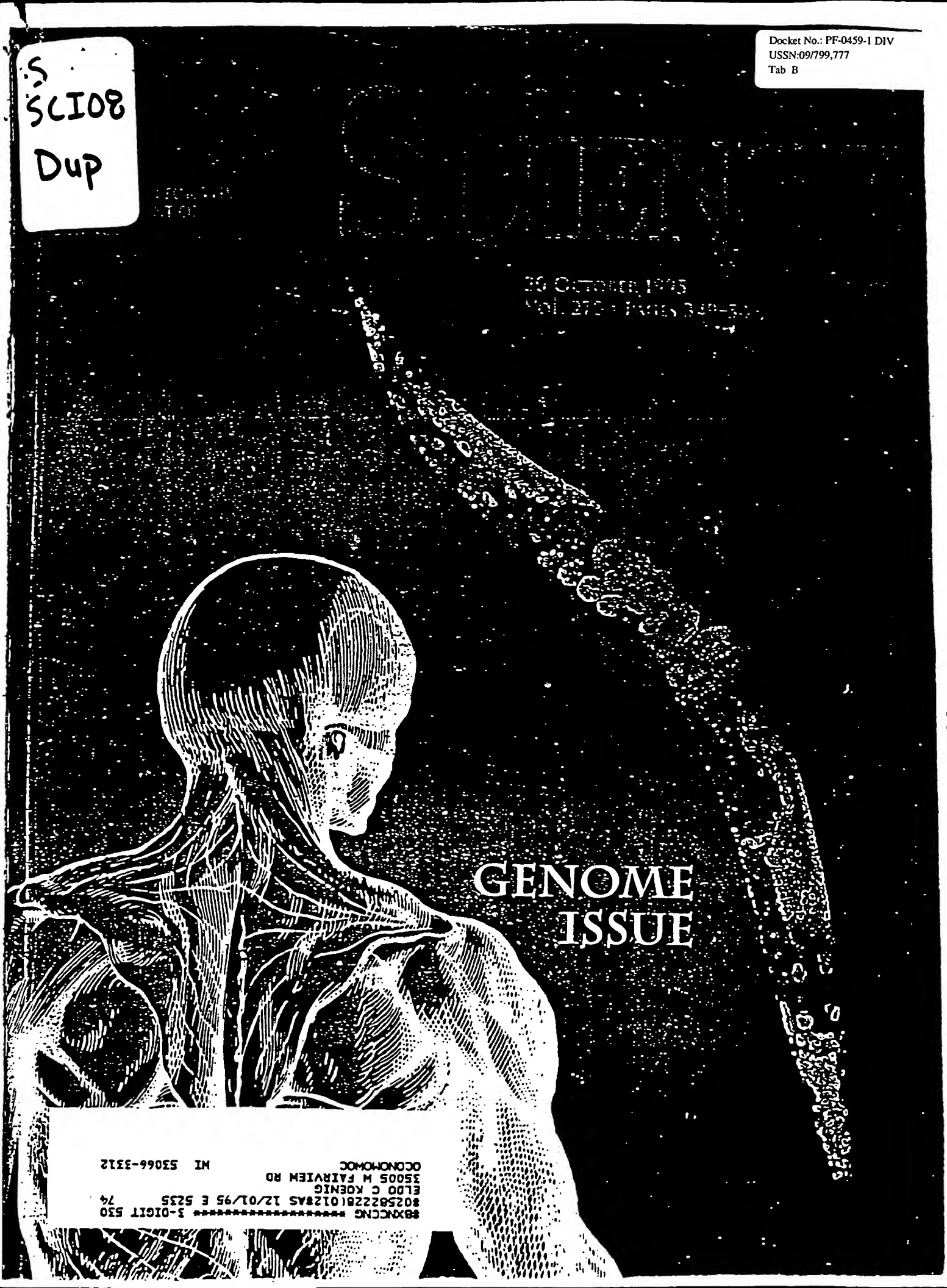
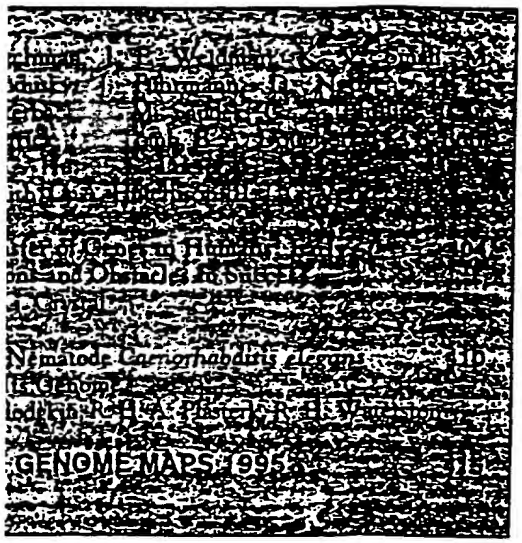


COVER

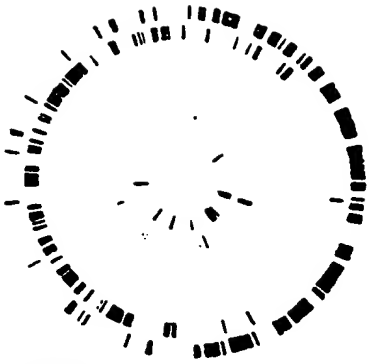
e Genome Project adds a new dimension to questions gene expression in humans and model systems. A art on page 415 summarizes progress in the *enorhabditis elegans* Genome Project and indicates me ways information about sequences can be used.

News stories, Articles, Perspectives, Policy Forums, and Reports focus on technological developments, clinical applications, and ethical concerns resulting from the burgeoning of genomic information. [*C. elegans* image: F. Maduro and D. Pilgrim, University of Alberta]



EPORTS

TECHNICAL COMMENTS



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Good things in small genomes

Indicates accompanying feature

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Axl1p sequence following Ser[208] and occurs within the domain of Axl1p that shows homology with hIDE (14). To delete the complete *STE23* sequence and create the *ste23Δ::URA3* mutation, polymerase chain reaction (PCR) primers (5'-TCGGAAGACCTCAT-TCTTGCTCATTTTGATATTGCTC- TGTAGATTG-TACTGAGAGTGCAC-3'; and 5'-GCTACAAACAGC-GTCGACTTGAATGCCCCGACATCTTCGACTGT-GCGGTATTTCACACCG-3') were used to amplify the *URA3* sequence of pRS316, and the reaction product was transformed into yeast for one-step gene replacement [R. Rothstein, *Methods Enzymol.* 194, 281 (1991)]. To create the *axl1Δ::LEU2* mutation contained on p114, a 5.0-kb Sal I fragment from pAXL1 was cloned into pUC19, and an internal 4.0-kb Hpa I–Xho I fragment was replaced with a *LEU2* fragment. To construct the *ste23Δ::LEU2* allele (a deletion corresponding to 931 amino acids) carried on p153, a *LEU2* fragment was used to replace the 2.8-kb Pml I–Ecl136 II fragment of *STE23*, which occurs within a 6.2-kb Hind III–Bgl II genomic fragment carried on pSP72 (Promega). To create YEp*MFA1*, a 1.6-kb Bam HI fragment containing *MFA1*, from pKK16 [K. Kuchler, R. E. Sterne, J. Thorner, *EMBO J.* 8, 3973 (1989)], was ligated into the Bam HI site of YEp351 [J. E. Hill, A. M. Myers, T. J. Koerner, A. Tzagoloff, *Yeast* 2, 163 (1986)].

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9. Single-letter abbreviations for the amino acid residues are as follows: A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.
10. A W303 1A derivative, SY2625 (*MATa ura3-1 leu2-3, 112 trp1-1 ade2-1 can1-100 sst1Δ mfa2Δ::FUS1-lacZ his3Δ::FUS1-HIS3*), was the parent strain for the mutant search. SY2625 derivatives for the mating assays, secreted pheromone assays, and the pulse-chase experiments included the following strains: Y49 (*ste22-1*), Y115 (*mfa1Δ::LEU2*), Y142 (*axl1::URA3*), Y173 (*axl1Δ::LEU2*), Y220 (*axl1::URA3 ste23Δ::URA3*), Y221 (*ste23Δ::URA3*), Y231 (*axl1Δ::LEU2 ste23Δ::LEU2*), and Y233 (*ste23Δ::LEU2*). *MATα* derivatives of SY2625 included the following strains: Y199 (SY2625 made *MATα*), Y278 (*ste22-1*), Y195 (*mfa1Δ::LEU2*), Y196 (*axl1Δ::LEU2*), and Y197 (*axl1::URA3*). The EG123 (*MATa leu2 ura3 trp1 can1 his4*) genetic background was used to create a set of strains for analysis of bud site selection. EG123 derivatives included the following strains: Y175 (*axl1Δ::LEU2*), Y223 (*axl1::URA3*), Y234 (*ste23Δ::LEU2*), and Y272 (*axl1Δ::LEU2 ste23Δ::LEU2*). *MATα* derivatives of EG123 included the following strains: Y214 (EG123 made *MATα*) and Y293 (*axl1Δ::LEU2*). All strains were generated by means of standard genetic or molecular methods involving the appropriate constructs (23). In particular, the *axl1 ste23* double mutant strains were created by crossing of the appropriate *MATa ste23* and *MATα axl1* mutants, followed by sporulation of the resultant diploid and isolation of the double mutant from nonparental di-type tetrads. Gene disruptions were confirmed with either PCR or Southern (DNA) analysis.
11. p129 is a YEp352 [J. E. Hill, A. M. Myers, T. J. Koerner, A. Tzagoloff, *Yeast* 2, 163 (1986)] plasmid containing a 5.5-kb Sal I fragment of pAXL1. p151 was derived from p129 by insertion of a linker at the Bgl II site within *AXL1*, which led to an in-frame insertion of the hemagglutinin (HA) epitope (DOYPYDVPDYA) (29) between amino acids 854 and 855 of the *AXL1* product. pC225 is a KS+ (Stratagene) plasmid containing a 0.5-kb Bam HI–Sst I fragment from pAXL1. Substitution mutations of the proposed active site of Axl1p were created with the use of pC225 and site-specific mutagenesis involving appropriate synthetic oligonucleotides (*axl1-H68A*, 5'-GTGCTCACAAAGCGCT-GCCAAACCGGC-3'; *axl1-E71A*, 5'-AAGAATCAT-GTGCGCACAAAGGTGCGC-3'; and *axl1-E71D*, 5'-AAGAATCATGTGATCACAAAGGTGCGC-3'). The mutations were confirmed by sequence analysis. After mutagenesis, the 0.4-kb Bam HI–Msc I fragment from the mutagenized pC225 plasmids was transferred into pAXL1 to create a set of pRS316 plasmids carrying different *AXL1* alleles, p124 (*axl1-H68A*), p130 (*axl1-E71A*), and p132 (*axl1-E71D*). Similarly, a set of HA-tagged alleles carried on YEp352 were created after replacement of the p151 Bam HI–Msc I fragment, to generate p161 (*axl1-E71A*), p162 (*axl1-H68A*), and p163 (*axl1-E71D*).

32. We thank J. Becker and S. Michaelis for providing a-factor antibodies; S. Michaelis for discussing unpublished results and helping with the pulse-chase experiments; J. Brown, J. Chant, and S. Sanders for their input concerning bud site selection experiments; M. Raymond, F. Tamanoi, and M. Whiteway for plasmids; M. Marra for providing the *STE23* genomic fragment; and H. Bussey, J. Brown, N. Davis, T. Favero, C. de Hoog, and S. Kim for comments on the manuscript. Supported by a grant to C.B. from the Natural Sciences and Engineering Research Council of Canada. Support for M.N.A. was from a California Tobacco-Related Disease Research Program postdoctoral fellowship (4FT-0083).

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Quantitative Monitoring of Gene Expression Patterns with a Complementary DNA Microarray

Mark Schena,* Dari Shalon,*† Ronald W. Davis, Patrick O. Brown‡

A high-capacity system was developed to monitor the expression of many genes in parallel. Microarrays prepared by high-speed robotic printing of complementary DNAs on glass were used for quantitative expression measurements of the corresponding genes. Because of the small format and high density of the arrays, hybridization volumes of 2 microliters could be used that enabled detection of rare transcripts in probe mixtures derived from 2 micrograms of total cellular messenger RNA. Differential expression measurements of 45 *Arabidopsis* genes were made by means of simultaneous, two-color fluorescence hybridization.

The temporal, developmental, topographical, histological, and physiological patterns in which a gene is expressed provide clues to its biological role. The large and expanding database of complementary DNA (cDNA) sequences from many organisms (*1*) presents the opportunity of defining these patterns at the level of the whole genome.

For these studies, we used the small flowering plant *Arabidopsis thaliana* as a model organism. *Arabidopsis* possesses many advantages for gene expression analysis, including the fact that it has the smallest genome of any higher eukaryote examined to date (*2*). Forty-five cloned *Arabidopsis* cDNAs (Table 1), including 14 complete sequences and 31 expressed sequence tags (ESTs), were used as gene-specific targets. We obtained the ESTs by selecting cDNA clones at random from an *Arabidopsis* cDNA library. Sequence analysis revealed that 28 of the 31 ESTs matched sequences in the database (Table 1). Three additional cDNAs from other organisms served as controls in the experiments.

The 48 cDNAs, averaging ~1.0 kb, were amplified with the polymerase chain reaction (PCR) and deposited into individual wells of a 96-well microtiter plate. Each sample was duplicated in two adjacent wells to allow the reproducibility of the arraying and hybridization process to be tested. Samples from the microtiter plate were printed onto glass microscope slides in an area measuring 3.5 mm by 5.5 mm with the use of a high-speed arraying machine (*3*). The arrays were processed by chemical and heat treatment to attach the DNA sequences to the glass surface and denature them (*3*). Three arrays, printed in a single lot, were used for the experiments here. A single microtiter plate of PCR products provides sufficient material to print at least 500 arrays.

Fluorescent probes were prepared from total *Arabidopsis* mRNA (*4*) by a single round of reverse transcription (*5*). The *Arabidopsis* mRNA was supplemented with human acetylcholine receptor (AChR) mRNA at a dilution of 1:10,000 (w/w) before cDNA synthesis, to provide an internal standard for calibration (*5*). The resulting fluorescently labeled cDNA mixture was hybridized to an array at high stringency (*6*) and scanned

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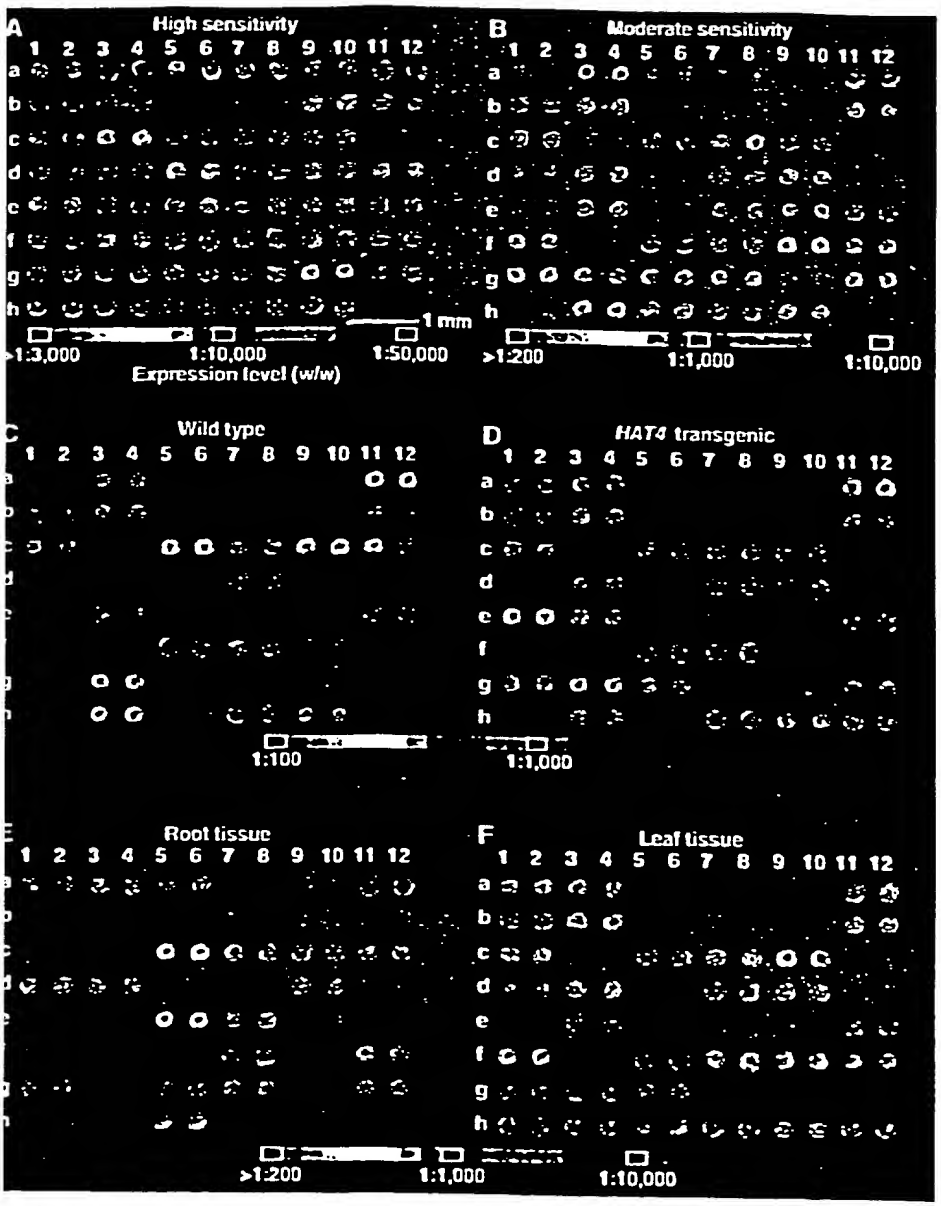
:h a laser (3). A high-sensitivity scan gave nals that saturated the detector at nearly of the *Arabidopsis* target sites (Fig. 1A). ilibration relative to the AChR mRNA ndard (Fig. 1A) established a sensitivity nit of ~1:50,000. No detectable hybridiza- n was observed to either the rat glucocor- oid receptor (Fig. 1A) or the yeast *TRP4* g. 1A) targets even at the highest scan- ng sensitivity. A moderate-sensitivity scan of the same array allowed linear detection of the more abundant transcripts (Fig. 1B). Quantitation of both scans revealed a range of expression levels spanning three orders of magnitude for the 45 genes tested (Table 2). RNA blots (7) for several genes (Fig. 2) corroborated the expression levels measured with the microarray to within a factor of 5 (Table 2).

Differential gene expression was investigated with a simultaneous, two-color hybridization scheme, which served to minimize experimental variation inherent in the comparison of independent hybridizations. Fluorescent probes were prepared from two mRNA sources with the use of reverse transcriptase in the presence of fluorescein- and lissamine-labeled nucleotide analogs, respectively (5). The two probes were then mixed together in equal proportions, hybridized to a single array, and scanned separately for fluorescein and lissamine emission after independent excitation of the two fluorophores (3).

To test whether overexpression of a single gene could be detected in a pool of total *Arabidopsis* mRNA, we used a microarray to analyze a transgenic line overexpressing the single transcription factor *HAT4* (8). Fluorescent probes representing mRNA from wild-type and *HAT4*-transgenic plants were labeled with fluorescein and lissamine, respectively; the two probes were then mixed and hybridized to a single array. An intense hybridization signal was observed at the position of the *HAT4* cDNA in the lissamine-specific scan (Fig. 1D), but not in the fluorescein-specific scan of the same array (Fig. 1C). Calibration with AChR mRNA added to the fluorescein and lissamine cDNA synthesis reactions at dilutions of 1:10,000 (Fig. 1C) and 1:100 (Fig. 1D), respectively, revealed a 50-fold elevation of *HAT4* mRNA in the transgenic line relative to its abundance in wild-type plants (Table 2). This magnitude of *HAT4* overexpression matched that inferred from the Northern (RNA) analysis within a factor of 2 (Fig. 2 and Table 2). Expression of all the other genes monitored on the array differed by less than a factor of 5 between *HAT4*-transgenic and wild-type plants (Fig 1, C



1. Gene expression monitored with the use of cDNA microarrays. Fluorescent scans represented in udocolor correspond to hybridization intensities. Color bars were calibrated from the signal obtained the use of known concentrations of human AChR mRNA in independent experiments. Numbers and rs on the axes mark the position of each cDNA. (A) High-sensitivity fluorescein scan after hybridization fluorescein-labeled cDNA derived from wild-type plants. (B) Same array as in (A) but scanned at erate sensitivity. (C and D) A single array was probed with a 1:1 mixture of fluorescein-labeled cDNA wild-type plants and lissamine-labeled cDNA from HAT4-transgenic plants. The single array was scanned successively to detect the fluorescein fluorescence corresponding to mRNA from wild-type s (C) and the lissamine fluorescence corresponding to mRNA from HAT4-transgenic plants (D). (E F) A single array was probed with a 1:1 mixture of fluorescein-labeled cDNA from root tissue and mine-labeled cDNA from leaf tissue. The single array was then scanned successively to detect the escein fluorescence corresponding to mRNAs expressed in roots (E) and the lissamine fluorescence sponding to mRNAs expressed in leaves (F).

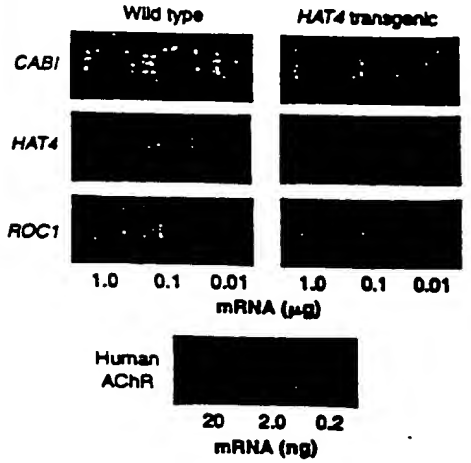


Fig. 2. Gene expression monitored with RNA (Northern) blot analysis. Designated amounts of mRNA from wild-type and *HAT4*-transgenic plants were spotted onto nylon membranes and probed with the cDNAs indicated. Purified human AChR mRNA was used for calibration.

and D, and Table 2). Hybridization of fluorescein-labeled glucocorticoid receptor cDNA (Fig. 1C) and lissamine-labeled *TRP4* cDNA (Fig. 1D) verified the presence of the negative control targets and the lack of optical cross talk between the two fluorophores.

To explore a more complex alteration in expression patterns, we performed a second two-color hybridization experiment with fluorescein- and lissamine-labeled probes prepared from root and leaf mRNA, respectively. The scanning sensitivities for the two fluorophores were normalized by matching the signals resulting from AChR mRNA, which was added to both cDNA synthesis reactions at a dilution of 1:1000 (Fig. 1, E and F). A comparison of the scans revealed widespread differences in gene expression between root and leaf tissue (Fig. 1, E and F). The mRNA from the light-regulated *CAB1* gene was ~500-fold more abundant in leaf (Fig. 1F) than in root tissue (Fig. 1E). The expression of 26 other genes differed between root and leaf tissue by more than a factor of 5 (Fig. 1, E and F).

The *HAT4*-transgenic line we examined has elongated hypocotyls, early flowering, poor germination, and altered pigmentation (*8*). Although changes in expression were observed for *HAT4*, large changes in expression were not observed for any of the other 44 genes we examined. This was somewhat surprising, particularly because comparative analysis of leaf and root tissue identified 27 differentially expressed genes. Analysis of an expanded set of genes may be required to identify genes whose expression changes upon *HAT4* overexpression; alternatively, a comparison of mRNA populations from specific tissues of wild-type and *HAT4*-transgenic plants may allow identification of downstream genes.

At the current density of robotic printing, it is feasible to scale up the fabrication process to produce arrays containing 20,000 cDNA targets. At this density, a single array would be sufficient to provide gene-specific targets encompassing nearly the entire repertoire of expressed genes in the *Arabidopsis* genome (*2*). The availability of 20,274 ESTs from *Arabidopsis* (*1*, *9*) would provide a rich source of templates for such studies.

The estimated 100,000 genes in the human genome (*10*) exceeds the number of *Arabidopsis* genes by a factor of 5 (*2*). This modest increase in complexity suggests that similar cDNA microarrays, prepared from the rapidly growing repertoire of human ESTs (*1*), could be used to determine the expression patterns of tens of thousands of human genes in diverse cell types. Coupling an amplification strategy to the reverse transcription reaction (*11*) could make it feasible to monitor expression even in minute tissue samples. A wide variety of acute and chronic physiological and pathological conditions might lead to characteristic changes in the patterns of gene expression in peripheral blood cells or other easily sampled tissues. In concert with cDNA microarrays for monitoring complex expression patterns, these tissues might therefore serve as sensitive in vivo sensors for clinical diagnosis. Microarrays of cDNAs could thus provide a useful link between human gene sequences and clinical medicine.

Table 1. Sequences contained on the cDNA microarray. Shown is the position, the known or putative function, and the accession number of each cDNA in the microarray (Fig. 1). All but three of the ESTs used in this study matched a sequence in the database. NADH, reduced form of nicotinamide adenine dinucleotide; ATPase, adenosine triphosphatase; GTP, guanosine triphosphate.

Position	cDNA	Function	Accession number
a1, 2	AChR	Human AChR	*
a3, 4	EST3	Actin	H36236
a5, 6	EST6	NADH dehydrogenase	Z27010
a7, 8	*AAC1*	Actin 1	M20016
a9, 10	EST12	Unknown	U36594†
a11, 12	EST13	Actin	T45783
b1, 2	*CAB1*	Chlorophyll a/b binding	M85150
b3, 4	EST17	Phosphoglycerate kinase	T44490
b5, 6	*GA4*	Gibberellic acid biosynthesis	L37126
b7, 8	EST19	Unknown	U36595†
b9, 10	*GBF-1*	G-box binding factor 1	X63894
b11, 12	EST23	Elongation factor	X52256
c1, 2	EST29	Aldolase	T04477
c3, 4	*GBF-2*	G-box binding factor 2	X63895
c5, 6	EST34	Chloroplast protease	R87034
c7, 8	EST35	Unknown	T14152
c9, 10	EST41	Catalase	T22720
c11, 12	rGR	Rat glucocorticoid receptor	M14053
d1, 2	EST42	Unknown	U36596†
d3, 4	EST45	ATPase	J04185
d5, 6	*HAT1*	Homeobox-leucine zipper 1	U09332
d7, 8	EST46	Light harvesting complex	T04063
d9, 10	EST49	Unknown	T76267
d11, 12	*HAT2*	Homeobox-leucine zipper 2	U09335
e1, 2	*HAT4*	Homeobox-leucine zipper 4	M90394
e3, 4	EST50	Phosphoribulokinase	T04344
e5, 6	*HAT5*	Homeobox-leucine zipper 5	M90416
e7, 8	EST51	Unknown	Z33675
e9, 10	*HAT22*	Homeobox-leucine zipper 22	U09336
e11, 12	EST52	Oxygen evolving	T21749
f1, 2	EST59	Unknown	Z34607
f3, 4	*KNAT1*	*Knotted*-like homeobox 1	U14174
f5, 6	EST60	RuBisCO small subunit	X14564
f7, 8	EST69	Translation elongation factor	T42799
f9, 10	*PPH1*	Protein phosphatase 1	U34803
f11, 12	EST70	Unknown	T44621
g1, 2	EST75	Chloroplast protease	T43698
g3, 4	EST78	Unknown	R65481
g5, 6	*ROC1*	Cyclophilin	L14844
g7, 8	EST82	GTP binding	X59152
g9, 10	EST83	Unknown	Z33795
g11, 12	EST84	Unknown	T45278
h1, 2	EST91	Unknown	T13832
h3, 4	EST96	Unknown	R64816
h5, 6	*SAR1*	Synaptobrevin	M90418
h7, 8	EST100	Light harvesting complex	Z18205
h9, 10	EST103	Light harvesting complex	X03909
h11, 12	*TRP4*	Yeast tryptophan biosynthesis	X04273

*Proprietary sequence of Stratagene (La Jolla, California). †No match in the database; novel EST.

Table 2. Gene expression monitoring by microarray and RNA blot analyses; tg, *HAT4*-transgenic. See Table 1 for additional gene information. Expression levels (w/w) were calibrated with the use of known amounts of human AChR mRNA. Values for the microarray were determined from microarray scans (Fig. 1); values for the RNA blot were determined from RNA blots (Fig. 2).

Gene	Expression level (w/w)	
	Microarray	RNA blot
CAB1	1:48	1:83
CAB1 (tg)	1:120	1:150
HAT4	1:8300	1:6300
HAT4 (tg)	1:150	1:210
ROC1	1:1200	1:1800
ROC1 (tg)	1:260	1:1300

EFERENCES AND NOTES

rrent EST database (dbEST release 091495) e National Center for Biotechnology Informa- thesda, MD) contains a total of 322,225 en- cluding 255,645 from the human genome ,044 from *Arabidopsis*. Access is available via rld Wide Web (http://www.ncbi.nlm.nih.gov). leyerowitz and R. E. Pruitt, *Science* 229, 1214 R. E. Pruitt and E. M. Meyerowitz, *J. Mol. Biol.* 9 (1986); I. Hwang *et al.*, *Plant J.* 1, 367 (1991); s *et al.*, *Plant Mol. Biol.* 24, 685 (1994); L. Le t *al.*, *Mol. Gen. Genet.* 245, 390 (1994).

on, thesis, Stanford University (1995); ——— O. Brown, in preparation. Microarrays were ed on poly-L-lysine–coated microscope Sigma) with a custom-built arraying machine ith one printing tip. The tip loaded 1 μl of PCR t (0.5 mg/ml) from 96-well microtiter plates posited ~0.005 μl per slide on 40 slides at a) of 500 μm. The printed slides were rehydrat- 2 hours in a humid chamber, snap-dried at for 1 min, rinsed in 0.1% SDS, and treated 05% succinic anhydride prepared in buffer ing of 50% 1-methyl-2-pyrrolidinone and onic acid. The cDNA on the slides was dena- distilled water for 2 min at 90°C immediately use. Microarrays were scanned with a laser ent scanner that contained a computer-con- (Y stage and a microscope objective. A mixed ultiline laser allowed sequential excitation of fluorophores. Emitted light was split accord- avelength and detected with two photomul- tubes. Signals were read into a PC with the use -bit analog-to-digital board. Additional details array fabrication and use may be obtained by of e-mail (pbrown@cmgm.stanford.edu).

usubel *et al.*, Eds., *Current Protocols in Mo- Biology* (Greene & Wiley Interscience, New 994), pp. 4.3.1–4.3.4.

onylated [poly(A)$^+$] mRNA was prepared from IA with the use of Oligotex-dT resin (Qiagen). e transcription (RT) reactions were carried out StrataScript RT-PCR kit (Stratagene) modified ws: 50-μl reactions contained 0.1 μg/μl of ipsis mRNA, 0.1 ng/μl of human AChR 0.05 μg/μl of oligo(dT) (21-mer), 1× first buffer, 0.03 U/μl of ribonuclease block, 500 oxyadenosine triphosphate (dATP), 500 μM uanosine triphosphate, 500 μM dTTP, 40 oxycytosine triphosphate (dCTP), 40 μM flu- n-12-dCTP (or lissamine-5-dCTP), and 0.03 StrataScript reverse transcriptase. Reactions ubated for 60 min at 37°C, precipitated with , and resuspended in 10 μl of TE (10 mM tris- l 1 mM EDTA, pH 8.0). Samples were then lor 3 min at 94°C and chilled on ice. The RNA graded by adding 0.25 μl of 10 N NaOH l by a 10-min incubation at 37°C. The sam- re neutralized by addition of 2.5 μl of 1 M)H 8.0) and 0.25 μl of 10 N HCl and precip- ith ethanol. Pellets were washed with 70% dried to completion in a speedvac, resus- in 10 μl of H_2O, and reduced to 3.0 μl in a ac. Fluorescent nucleotide analogs were ob- om New England Nuclear (DuPont).

ation reactions contained 1.0 μl of fluorescent nthesis product (5) and 1.0 μl of hybridization 10× saline sodium citrate (SSC) and 0.2% he 2.0-μl probe mixtures were aliquoted onto oarray surface and covered with cover slips round). Arrays were transferred to a hybrid- chamber (3) and incubated for 18 hours at rrays were washed for 5 min at room temper- 5°C) in low-stringency wash buffer (1× SSC % SDS), then for 10 min at room temperature tringency wash buffer (0.1× SSC and 0.1% rrays were scanned in 0.1× SSC with the use rescence laser-scanning device (3).

; of poly(A)$^+$ mRNA (4, 5) were spotted onto embranes (Nytran) and crosslinked with ul- light with the use of a Stratalinker 1800 ene). Probes were prepared by random with the use of a Prime-It II kit (Stratagene) in ence of [^{32}P]dATP. Hybridizations were car- according to the instructions of the manu- facturer. Quantitation was performed on a Phos- phorImager (Molecular Dynamics).

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Gene Therapy in Peripheral Blood Lymphocytes and Bone Marrow for ADA$^-$ Immunodeficient Patients

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Adenosine deaminase (ADA) deficiency results in severe combined immunodeficiency, the first genetic disorder treated by gene therapy. Two different retroviral vectors were used to transfer ex vivo the human ADA minigene into bone marrow cells and peripheral blood lymphocytes from two patients undergoing exogenous enzyme replacement therapy. After 2 years of treatment, long-term survival of T and B lymphocytes, marrow cells, and granulocytes expressing the transferred ADA gene was demonstrated and resulted in normalization of the immune repertoire and restoration of cellular and humoral immunity. After discontinuation of treatment, T lymphocytes, derived from transduced peripheral blood lymphocytes, were progressively replaced by marrow-derived T cells in both patients. These results indicate successful gene transfer into long-lasting progenitor cells, producing a functional multilineage progeny.

Severe combined immunodeficiency associated with inherited deficiency of ADA (*1*) is usually fatal unless affected children are kept in protective isolation or the immune system is reconstituted by bone marrow transplantation from a human leukocyte antigen (HLA)–identical sibling donor (*2*). This is the therapy of choice, although it is available only for a minority of patients. In recent years, other forms of therapy have been developed, including transplants from haploidentical donors (*3*, *4*), exogenous enzyme replacement (*5*), and somatic-cell gene therapy (*6*–*9*).

We previously reported a preclinical model in which ADA gene transfer and expression successfully restored immune functions in human ADA-deficient (ADA$^-$) peripheral blood lymphocytes (PBLs) in immunodeficient mice in vivo (*10*, *11*). On the basis of these preclinical results, the clinical application of gene therapy for the treatment of ADA$^-$ SCID (severe combined immunodeficiency disease) patients who previously failed exogenous enzyme replacement therapy was approved by our Institutional Ethical Committees and by the Italian National Committee for Bioethics (*12*). In addition to evaluating the safety and efficacy of the gene therapy procedure, the aim of the study was to define the relative role of PBLs and hematopoietic stem cells in the long-term reconstitution of immune functions after retroviral vector–mediated ADA gene transfer. For this purpose, two structurally identical vectors expressing the human ADA complementary DNA (cDNA), distinguishable by the presence of alternative restriction sites in a nonfunctional region of the viral long-terminal repeat (LTR), were used to transduce PBLs and bone marrow (BM) cells independently. This procedure allowed identification of the origin of

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